

SCORE Search Results Details for Application 10759514 and Search Result us-10-759-514-3.rge.

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 06:16:29 ; Search time 558.626 Seconds
(without alignments)
2442.141 Million cell updates/sec

Title: US-10-759-514-3
Perfect score: 24
Sequence: 1 ccgggagagccatagtgtctgcg 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	24	100.0	37	6	E25770	E25770 Method for
2	24	100.0	50	6	E44269	E44269 Oligo-DNA s
c 3	24	100.0	53	6	I44586	I44586 Sequence 15
c 4	24	100.0	53	6	I70991	I70991 Sequence 15
5	24	100.0	102	6	BD092000	BD092000 Potentiat
6	24	100.0	102	6	BD006783	BD006783 Method fo
7	24	100.0	109	6	AR655267	AR655267 Sequence
8	24	100.0	109	6	AR655268	AR655268 Sequence
9	24	100.0	109	6	AR655269	AR655269 Sequence
10	24	100.0	110	13	AY690640	AY690640 Hepatitis
11	24	100.0	110	13	AY690641	AY690641 Hepatitis
12	24	100.0	110	13	AY690642	AY690642 Hepatitis
13	24	100.0	110	13	AY690643	AY690643 Hepatitis
14	24	100.0	110	13	AY690644	AY690644 Hepatitis
15	24	100.0	110	13	AY690645	AY690645 Hepatitis
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17	24	100.0	110	13	AY690647	AY690647 Hepatitis
18	24	100.0	110	13	AY690648	AY690648 Hepatitis
19	24	100.0	110	13	AY690649	AY690649 Hepatitis
20	24	100.0	110	13	AY690650	AY690650 Hepatitis
21	24	100.0	110	13	AY690651	AY690651 Hepatitis
22	24	100.0	110	13	AY690652	AY690652 Hepatitis
23	24	100.0	110	13	AY690653	AY690653 Hepatitis
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25	24	100.0	110	13	AY690655	AY690655 Hepatitis
26	24	100.0	110	13	AY690656	AY690656 Hepatitis
27	24	100.0	112	6	AR655272	AR655272 Sequence
28	24	100.0	116	13	HPCCHA12	M74254 Hepatitis C
29	24	100.0	116	13	HPCCHA13	M74255 Hepatitis C
30	24	100.0	123	13	HPCUT6CLN	M94468 Hepatitis C
31	24	100.0	125	13	HPCCHA10	M74252 Hepatitis C
32	24	100.0	131	13	CS001589	CS001589 Sequence
33	24	100.0	131	13	CS001590	CS001590 Sequence
34	24	100.0	131	13	CS001591	CS001591 Sequence
35	24	100.0	131	13	CS001592	CS001592 Sequence
36	24	100.0	131	13	CS001593	CS001593 Sequence
37	24	100.0	131	13	CS001594	CS001594 Sequence
c 38	24	100.0	140	6	E10301	E10301 Anti-sense
c 39	24	100.0	140	13	AY766490	AY766490 Hepatitis
40	24	100.0	142	13	S72378	S72378 {5' region}
41	24	100.0	148	13	HPCCHA6	M74248 Hepatitis C
42	24	100.0	149	13	HPCEB1	D10114 Hepatitis C
43	24	100.0	149	13	HPCEB11	D10118 Hepatitis C
44	24	100.0	149	13	HPCEB12	D10119 Hepatitis C
45	24	100.0	149	13	HPCEB13	D10120 Hepatitis C

ALIGNMENTS

RESULT 1

E25770

LOCUS E25770 37 bp DNA linear PAT 18-JUN-2001.

DEFINITION Method for assaying HCV gene by real time detection PCR method and primer and probe to be used therein.

ACCESSION E25770

VERSION E25770.1 GI:13024958

KEYWORDS JP 1999103899-A/1.

SOURCE unidentified

ORGANISM unidentified

unclassified.

REFERENCE 1 (bases 1 to 37)

AUTHORS Michinori,O., Ryuji,K. and Aki,A.

TITLE Method for assaying HCV gene by real time detection PCR method and primer and probe to be used therein

JOURNAL Patent: JP 1999103899-A 1 20-APR-1999;
TOKYO MET GOV RINSHO IGAKU SOGO KENKYUSHO,SRL INC

COMMENT OS Unidentified
PN JP 1999103899-A/1
PD 20-APR-1999
PF 30-SEP-1997 JP 1997283042
PR
PI MICHINORI OBARA,RYUJI KAWAGUCHI,AKI ABE
PC C12Q1/70,C12N15/09,G01N21/78,G01N33/58,C12N15/00 CC
FH Key Location/Qualifiers
FT source 1. .37
FT /organism='Unidentified'.

FEATURES Location/Qualifiers
source 1. .37
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
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Db 10 CCGGGAGAGCCATAGTGGTCTGCG 33

RESULT 2

E44269

LOCUS E44269 50 bp DNA linear PAT 31-JAN-2002

DEFINITION Oligo-DNA strongly binding to HCVRNA and process for conveniently producing the DNA.

ACCESSION E44269

VERSION E44269.1 GI:18629221

KEYWORDS JP 2000210090-A/13.

SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 50)

AUTHORS Taya,T., Ishiguro,T. and Saito,H.

TITLE Oligo-DNA strongly binding to HCVRNA and process for conveniently producing the DNA

JOURNAL Patent: JP 2000210090-A 13 02-AUG-2000;
TOSOH CORP

COMMENT OS Artificial Sequence
PN JP 2000210090-A/13
PD 02-AUG-2000
PF 19-NOV-1999 JP 1999329333
PR
PI TOSHITAKA TAYA,TAKAHIKO ISHIGURO,HISAKAZU SAITO PC
C12N15/09,C12Q1/68,C12Q1/70,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .50
FT /organism='Artificial Sequence'.

FEATURES Location/Qualifiers
source 1. .50
/organism="synthetic construct"

/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
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Db 26 CCGGGAGAGCCATAGTGGTCTGCG 49

RESULT 3

I44586/c

LOCUS I44586 53 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence (15 from patent US 5635352.

ACCESSION I44586

VERSION I44586.1 GI:2469299

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 53)

AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.

TITLE Solution phase nucleic acid sandwich assays having reduced background noise

JOURNAL Patent: US 5635352-A 15 03-JUN-1997;

FEATURES Location/Qualifiers

source 1. .53

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
|||||
Db 44 CCGGGAGAGCCATAGTGGTCTGCG 21

RESULT 4

I70991/c

LOCUS I70991 53 bp DNA linear PAT 03-APR-1998

DEFINITION Sequence (15 from patent US 5681697)

ACCESSION I70991

VERSION I70991.1 GI:3007126

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 53)

AUTHORS Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.

TITLE Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor

JOURNAL Patent: US 5681697-A 15 28-OCT-1997;

FEATURES Location/Qualifiers

source 1. .53

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
|||||
Db 44 CCGGGAGAGCCATAGTGGTCTGCG 21

RESULT 5

BD092000

LOCUS BD092000 102 bp RNA linear PAT 27-AUG-2002

DEFINITION Potentiated nucleic acid amplification method.

ACCESSION BD092000

VERSION BD092000.1 GI:22637611

KEYWORDS WO 0075371-A/7.

SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 102)

AUTHORS Ishizuka,T., Ishiguro,T., Saito,J. and Sakai,T.

TITLE Potentiated nucleic acid amplification method

JOURNAL Patent: WO 0075371-A 7 14-DEC-2000;
TOSOH CORP,TETSUYA ISHIZUKA,TAKAHIKO ISHIGURO,JUICHI SAITO, TOMOMI
SAKAI

COMMENT OS Artificial Sequence

PN WO 0075371-A/7

PD 14-DEC-2000

PF 05-JUN-2000 WO 2000JP003647

PR 04-JUN-1999 JP 99P 157653

PI TETSUYA ISHIZUKA,TAKAHIKO ISHIGURO,JUICHI SAITO,TOMOMI SAKAI

PC C12Q1/68,C12N15/09,G01N33/542,G01N33/566

CC Human C-type hepatitis virus synthetic RNA(WQ-RNA) FH Key

Location/Qualifiers.

FEATURES Location/Qualifiers

source 1. .102

/organism="synthetic construct"

/mol_type="genomic RNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 24; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGAGAGCCATAGTGGTCTGCG 24
|||||
Db 13 CCGGGAGAGCCATAGTGGTCTGCG 36

RESULT 6

BD006783

LOCUS BD006783 102 bp RNA linear PAT 31-JAN-2002

DEFINITION Method for amplifying potentiated nucleic acid.

ACCESSION BD006783

VERSION BD006783.1 GI:18635154

KEYWORDS JP 2001046099-A/7.

SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1 (bases 1 to 102)

AUTHORS Ishizuka,T., Ishiguro,T., Saito,J. and Sakai,T.

TITLE Method for amplifying potentiated nucleic acid

JOURNAL Patent: JP 2001046099-A 7 20-FEB-2001;

SCORE Search Results Details for Application 10759 Result us-10-759-514-6.rge.

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This page gives you Search Results detail for the Application 10759514 and Search Result us-10-759-514-
[start](#)

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 7, 2006, 06:16:29 ; Search time 512.074 Seconds
(without alignments)
2442.141 Million cell updates/sec

Title: US-10-759-514-6
Perfect score: 22
Sequence: 1 ttggcaacagtggcatgcaccg 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query

No.	Score	Match	Length	DB	ID	Description
c 1	22	100.0	1337	13	AF059603	AF059603 Wheat ros
c 2	22	100.0	5557	6	CQ830721	CQ830721 Sequence
c 3	22	100.0	5557	6	CQ832100	CQ832100 Sequence
c 4	22	100.0	48502	7	LAMCG	J02459 Bacteriopha
c 5	19.4	88.2	44139	2	AY190942	AY190942 Drosophil
c 6	18.8	85.5	30844	15	AC158186	AC158186 Selaginel
7	18.8	85.5	104771	9	AL603830	AL603830 Mouse DNA
8	18.8	85.5	206431	14	AC161885	AC161885 Gallus ga
9	18.8	85.5	244279	14	AC163712	AC163712 Gallus ga
10	18.8	85.5	248883	14	AC098544	AC098544 Rattus no
11	18.8	85.5	259215	14	AC118088	AC118088 Rattus no
12	18.8	85.5	262976	14	AC120483	AC120483 Rattus no
c 13	18.8	85.5	264908	9	AC096627	AC096627 Mus muscu
14	18.4	83.6	110000	1	BA000023_21	Continuation (22 o
15	18.4	83.6	110000	1	BA000023_22	Continuation (23 o
16	18.4	83.6	145993	8	AC098972	AC098972 Homo sapi
17	18.4	83.6	167304	9	AL928678	AL928678 Mouse DNA
c 18	18.4	83.6	169111	14	CR954168	CR954168 Danio rer
19	18.4	83.6	197839	9	AL845466	AL845466 Mouse DNA
20	18.4	83.6	207127	14	AC069496	AC069496 Homo sapi
c 21	18.4	83.6	213005	8	AP005059	AP005059 Homo sapi
22	18.4	83.6	220618	14	AC131892	AC131892 Atelerix
c 23	18.4	83.6	237739	14	AC134520	AC134520 Atelerix
24	17.8	80.9	905	10	BV576244	BV576244 G591P6073
c 25	17.8	80.9	32931	15	AC158190	AC158190 Selaginel
26	17.8	80.9	37165	15	AC158184	AC158184 Selaginel
27	17.8	80.9	39857	8	AC002522	AC002522 Homo sapi
28	17.8	80.9	44873	8	AC004461	AC004461 Homo sapi
29	17.8	80.9	59030	5	BX324184	BX324184 Zebrafish
30	17.8	80.9	97351	8	AC015853	AC015853 Homo sapi
31	17.8	80.9	108400	8	HUMDGCRCEN	L77570 Homo sapien
c 32	17.8	80.9	110000	1	BA000019_08	Continuation (9 of
33	17.8	80.9	110000	15	CR382131_32	Continuation (33 o
34	17.8	80.9	114540	8	AC107426	AC107426 Homo sapi
35	17.8	80.9	125630	14	AC090650	AC090650 Arabidops
c 36	17.8	80.9	149939	5	AL935281	AL935281 Zebrafish
c 37	17.8	80.9	153284	8	AC078925	AC078925 Homo sapi
c 38	17.8	80.9	157327	14	CR450752	CR450752 Danio rer
39	17.8	80.9	157904	8	AC108486	AC108486 Homo sapi
40	17.8	80.9	159868	8	AC122129	AC122129 Homo sapi
c 41	17.8	80.9	159876	8	HS253P07	AL354000 Homo from
c 42	17.8	80.9	159994	8	AC157498	AC157498 Pan trogl
c 43	17.8	80.9	160256	5	BX950187	BX950187 Zebrafish
44	17.8	80.9	160583	14	AC154944	AC154944 Monodelph
45	17.8	80.9	169665	14	AC144566	AC144566 Homo sapi

ALIGNMENTS

RESULT 1

AF059603/c

LOCUS AF059603 1337 bp mRNA linear VRL 30-JAN-2000

DEFINITION Wheat rosette stunt virus nucleocapsid protein (N) mRNA, partial cds.

ACCESSION AF059603

VERSION AF059603.1 GI:6815246

KEYWORDS .

SOURCE Wheat rosette stunt virus

ORGANISM Wheat rosette stunt virus

Viruses; ssRNA negative-strand viruses; Mononegavirales;
Rhabdoviridae; unclassified Rhabdoviridae.

REFERENCE 1 (bases 1 to 1337)
AUTHORS Gong,Z.X.
TITLE Direct Submission
JOURNAL Submitted (15-APR-1998) Virology Laboratory, Shanghai Institute of Biochemistry, Chinese Academy of Science, 320 Yue Yang Rd., Shanghai 200031, P.R. China

FEATURES Location/Qualifiers
source 1. .1337
/organism="Wheat rosette stunt virus"
/mol_type="mRNA"
/db_xref="taxon:75890"
gene <1. .1337
/gene="N"
CDS <1. .1209
/gene="N"
/codon_start=1
/product="nucleocapsid protein"
/protein_id="AAF28467.1"
/db_xref="GI:6815247"
/translation="TFTKGDAERWVSTTKKASDSAFWLEVEGNSMTAPNGSKPSLAVI
VHLSSSVEVIFLGLSSSFRRSLICFRNYFIVILYHAYDNLLMSNLLILNKLFSWLHQI
KSRMMLAKSHRHPLDCLFVCQESYSSYTFCHRLRLRHVIIRNLLAYRPIVFLIYKVD
DTVLRCTGDSMILRHIVIVHRIYIYIIICINRVACSATVAHRRYGRARRHVVCNVVR
LAGELPIVRVLNDFQLLPILHIFCMREFVPPPTDHLSTLYATVPRLLCAGATLQTSFSV
HATVANDLPRNWLASYRCKNSPPHIKSIRSLPISVVISIFIIFMIPRKNLPSLLAR
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LQTIPVSNIK"

ORIGIN

Query Match 100.0%; Score 22; DB 13; Length 1337;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCAACAGTGGCATGCACCG 22
|||||
Db 845 TTGGCAACAGTGGCATGCACCG 824

RESULT 2

CQ830721/c
LOCUS CQ830721 5557 bp DNA linear PAT 12-JUL-2004
DEFINITION Sequence 24 from Patent WO2004055215.
ACCESSION CQ830721
VERSION CQ830721.1 GI:50251007
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Otte,A.P. and van Blokland,H.J.
TITLE A method for improving protein production
JOURNAL Patent: WO 2004055215-A 24 01-JUL-2004;
Chromagenics B.V. (NL)

FEATURES Location/Qualifiers
source 1. .5557
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="lambda fragment 22425-27972"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 5557;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCAACAGTGGCATGCACCG 22
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 Db 1968 TTGGCAACAGTGGCATGCACCG 1947

RESULT 3

CQ832100/c

LOCUS CQ832100 5557 bp DNA linear PAT 29-JUL-2004

DEFINITION Sequence 9 from Patent WO2004056986.

ACCESSION CQ832100

VERSION CQ832100.1 GI:50831814

KEYWORDS .

SOURCE Bacteriophage lambda

ORGANISM Bacteriophage lambda

Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;

Lambda-like viruses.

REFERENCE 1

AUTHORS Otte,A.P., Kwaks,T.H. and Sewalt,R.G.

TITLE Means and methods for producing a protein through chromatin openers that are capable of rendering chromatin more accessible to transcription factors

JOURNAL Patent: WO 2004056986-A 9 08-JUL-2004;

Chromagenics B.V. (NL)

FEATURES Location/Qualifiers

source 1. .5557

/organism="Bacteriophage lambda"

/mol_type="unassigned DNA"

/db_xref="taxon:10710"

ORIGIN

Query Match 100.0%; Score 22; DB 6; Length 5557;

Best Local Similarity 100.0%; Pred. No. 4;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGGCAACAGTGGCATGCACCG 22
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 Db 1968 TTGGCAACAGTGGCATGCACCG 1947

RESULT 4

LAMCG/c

LOCUS LAMCG 48502 bp DNA circular PHG 17-APR-2002

DEFINITION Bacteriophage lambda, complete genome.

ACCESSION J02459 M17233 M24325 V00636 X00906

VERSION J02459.1 GI:215104

KEYWORDS DNA-binding protein; circular; coat protein; complete genome; origin of replication; repressor; unidentified reading frame.

SOURCE Bacteriophage lambda

ORGANISM Bacteriophage lambda

Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;

Lambda-like viruses.

REFERENCE 2 (bases 1 to 12)

AUTHORS Wu,R. and Taylor,E.

TITLE Nucleotide sequence analysis of DNA. II. Complete nucleotide sequence of the cohesive ends of bacteriophage lambda DNA

JOURNAL J. Mol. Biol. 57 (3), 491-511 (1971)

PUBMED 4931680

REFERENCE 3 (bases 45493 to 45963)

AUTHORS Imada,M. and Tsugita,A.

TITLE Amino acid sequence of lambda phage endolysin

JOURNAL Nature New Biol. 233, 230-231 (1971)

REFERENCE 4 (sites)

AUTHORS Weigel,P.H., Englund,P.T., Murray,K. and Old,R.W.

TITLE The 3'-terminal nucleotide sequences of bacteriophage lambda DNA
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 70 (4), 1151-1155 (1973)
 PUBMED 4515613
 REFERENCE 5 (bases 38597 to 38672)
 AUTHORS Dahlberg, J.E. and Blattner, F.R.
 TITLE In vitro transcription products of lambda DNA: Nucleotide sequences and regulatory sites
 JOURNAL (in) Fox, C.F. and Robinson, W.S. (Eds.);
 VIRUS RESEARCH. PROCEEDINGS OF 1973 ICN-UCLA SYMPOSIUM: 533-544;
 Academic Press, New York (1973)
 REFERENCE 6 (bases 37945 to 38027)
 AUTHORS Maniatis, T., Ptashne, M., Backman, K., Kield, D., Flashman, S.,
 Jeffrey, A. and Maurer, R.
 TITLE Recognition sequences of repressor and polymerase in the operators of bacteriophage lambda
 JOURNAL Cell 5 (2), 109-113 (1975)
 PUBMED 1095210
 REFERENCE 7 (bases 35583 to 35600)
 AUTHORS Kleid, D.G., Agarwal, K.L. and Khorana, H.G.
 TITLE The nucleotide sequence in the promoter region of the gene N in bacteriophage lambda
 JOURNAL J. Biol. Chem. 250 (14), 5574-5582 (1975)
 PUBMED 167018
 REFERENCE 8 (bases 35434 to 35618)
 AUTHORS Dahlberg, J.E. and Blattner, F.R.
 TITLE Sequence of the promoter-operator proximal region of the major leftward RNA of bacteriophage lambda
 JOURNAL Nucleic Acids Res. 2 (9), 1441-1458 (1975)
 PUBMED 1178525
 REFERENCE 9 (bases 37945 to 38018)
 AUTHORS Maniatis, T., Jeffrey, A. and Kleid, D.G.
 TITLE Nucleotide sequence of the rightward operator of phage lambda
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 72 (3), 1184-1188 (1975)
 PUBMED 1055375
 REFERENCE 10 (bases 44588 to 44773)
 AUTHORS Sklar, J., Yot, P. and Weissman, S.M.
 TITLE Determination of genes, restriction sites, and DNA sequences surrounding the 6S RNA template of bacteriophage lambda
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 72 (5), 1817-1821 (1975)
 PUBMED 1098044
 REFERENCE 11 (bases 37905 to 37989)
 AUTHORS Walz, A., Pirrotta, V. and Ineichen, K.
 TITLE Lambda repressor regulates the switch between PR and Prm promoters
 JOURNAL Nature 262 (5570), 665-669 (1976)
 PUBMED 958438
 REFERENCE 12 (bases 37946 to 38039)
 AUTHORS Smith, G.R., Eisen, H., Reichardt, L. and Hedgepeth, J.
 TITLE Deletions of lambda phage locating a prm mutation within the rightward operator
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 73 (3), 712-716 (1976)
 PUBMED 1062780
 REFERENCE 13 (bases 35578 to 35667; 37903 to 38027)
 AUTHORS Ptashne, M., Backman, K., Humayun, M.Z., Jeffrey, A., Maurer, R., Meyer, B. and Sauer, R.T.
 TITLE Autoregulation and function of a repressor in bacteriophage lambda
 JOURNAL Science 194 (4261), 156-161 (1976)
 PUBMED 959843
 REFERENCE 14 (bases 35578 to 35667)
 AUTHORS Humayun, Z., Jeffrey, A. and Ptashne, M.
 TITLE Completed DNA sequences and organization of repressor-binding sites in the operators of phage lambda
 JOURNAL J. Mol. Biol. 112 (2), 265-277 (1977)
 PUBMED 875019
 REFERENCE 15 (bases 38610 to 38732)

AUTHORS Scherer,G., Hobom,G. and Kossel,H.
 TITLE DNA base sequence of the po promoter region of phage lamdba
 JOURNAL Nature 265 (5590), 117-121 (1977)
 PUBMED 834253
 REFERENCE 16 (bases 38041 to 38241)
 AUTHORS Roberts,T.M., Shimatake,H., Brady,C. and Rosenberg,M.
 TITLE Sequence of Cro gene of bacteriophage lambda
 JOURNAL Nature 270 (5634), 274-275 (1977)
 PUBMED 593347
 REFERENCE 17 (bases 27616 to 28935)
 AUTHORS Davies,R.W., Schreier,P.H. and Buchel,D.E.
 TITLE Nucleotide sequence of the attachment site of coliphage lambda
 JOURNAL Nature 270 (5639), 757-760 (1977)
 PUBMED 593399
 REFERENCE 18 (bases 37206 to 37263; 37914 to 37970)
 AUTHORS Humayun,Z.
 TITLE DNA sequence at the end of the cI gene in bacteriophage lambda
 JOURNAL Nucleic Acids Res. 4 (7), 2137-2143 (1977)
 PUBMED 909767
 REFERENCE 19 (bases 27617 to 27934)
 AUTHORS Landy,A. and Ross,W.
 TITLE Viral integration and excision: structure of the lambda att sites
 JOURNAL Science 197 (4309), 1147-1160 (1977)
 PUBMED 331474
 REFERENCE 20 (bases 39062 to 39170)
 AUTHORS Denniston-Thompson,K., Moore,D.D., Kruger,K.E., Furth,M.E. and Blattner,F.R.
 TITLE Physical structure of the replication origin of bacteriophage lambda
 JOURNAL Science 198 (4321), 1051-1056 (1977)
 PUBMED 929187
 REFERENCE 21 (bases 44467 to 44807)
 AUTHORS Sklar,J.L.
 TITLE Structure and function of two regions of DNA controlling the synthesis of prokaryotic RNAs
 JOURNAL Thesis (1977)
 REFERENCE 22 (sites)
 AUTHORS Adhya,S. and Gottesman,M.
 TITLE Control of transcription termination
 JOURNAL Annu. Rev. Biochem. 47, 967-996 (1978)
 PUBMED 354508
 REFERENCE 23 (bases 13 to 72; 48391 to 48502)
 AUTHORS Nichols,B.P. and Donelson,J.E.
 TITLE 178-Nucleotide sequence surrounding the cos site of bacteriophage lambda DNA
 JOURNAL J. Virol. 26 (2), 429-434 (1978)
 PUBMED 666898
 REFERENCE 24 (bases 37938 to 38016; 35589 to 35666)
 AUTHORS Flashman,S.M.
 TITLE Mutational analysis of the operators of bacteriophage lambda
 JOURNAL Mol. Gen. Genet. 166 (1), 61-73 (1978)
 PUBMED 368570
 REFERENCE 25 (bases 37990 to 38982)
 AUTHORS Schwarz,E., Scherer,G., Hobom,G. and Kossel,H.
 TITLE Nucleotide sequence of cro, cII and part of the O gene in phage lambda DNA
 JOURNAL Nature 272 (5652), 410-414 (1978)
 PUBMED 264238
 REFERENCE 26 (bases 38212 to 38362)
 AUTHORS Rosenberg,M., Court,D., Shimatake,H., Brady,C. and Wulff,D.L.
 TITLE The relationship between function and DNA sequence in an intercistronic regulatory region in phage lambda
 JOURNAL Nature 272 (5652), 414-423 (1978)
 PUBMED 634366

REFERENCE 27 (bases 37224 to 37940)
AUTHORS Sauer,R.T.
TITLE DNA sequence of the bacteriophage gama cI gene
JOURNAL Nature 276 (5685), 301-302 (1978)
PUBMED 714163

REFERENCE 28 (bases 38597 to 39688)
AUTHORS Scherer,G.
TITLE Nucleotide sequence of the O gene and of the origin of replication in bacteriophage lambda DNA
JOURNAL Nucleic Acids Res. 5 (9), 3141-3156 (1978)
PUBMED 704348

REFERENCE 29 (bases 29711 to 29811; 31043 to 31058)
AUTHORS Davies,R.W., Schreier,P.H. and Buchel,D.E.
TITLE Determination of the endpoints of partial deletion mutants of the attachment site of bacteriophage lambda by DNA sequencing
JOURNAL Nucleic Acids Res. 5 (9), 3209-3218 (1978)
PUBMED 704352

REFERENCE 30 (bases 21661 to 31129)
AUTHORS Hoess,R.H. and Landy,A.
TITLE Structure of the lambda att sites generated by int-dependent deletions
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 75 (11), 5437-5441 (1978)
PUBMED 364480

REFERENCE 31 (bases 38453 to 38500)
AUTHORS Sprague,K.U., Faulds,D.H. and Smith,G.R.
TITLE A single base-pair change creates a Chi recombinational hotspot in bacteriophage lambda
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 75 (12), 6182-6186 (1978)
PUBMED 282634

REFERENCE 32 (bases 27711 to 27826)
AUTHORS Ross,W., Landy,A., Kikuchi,Y. and Nash,H.
TITLE Interaction of int protein with specific sites on lambda att DNA
JOURNAL Cell 18 (2), 297-307 (1979)
PUBMED 159130

REFERENCE 33 (bases 38008 to 39328)
AUTHORS Moore,D.D., Denniston-Thompson,K., Kruger,K.E., Furth,M.E., Williams,B.G., Daniels,D.L. and Blattner,F.R.
TITLE Dissection and comparative anatomy of the origins of replication of lambdoid phages
JOURNAL Cold Spring Harb. Symp. Quant. Biol. 43 Pt 1, 155-163 (1979)
PUBMED 157834

REFERENCE 34 (bases 38470 to 39189)
AUTHORS Hobom,G., Grosschedl,R., Lusky,M., Scherer,G., Schwarz,E. and Kossel,H.
TITLE Functional analysis of the replicator structure of lambdoid bacteriophage DNAs
JOURNAL Cold Spring Harb. Symp. Quant. Biol. 43 Pt 1, 165-178 (1979)
PUBMED 157835

REFERENCE 35 (bases 38453 to 38500)
AUTHORS Smith,G.R., Faulds,D.H. and Sprague,K.U.

Query Match 100.0%; Score 22; DB 7; Length 48502;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 24388 TTGGCAACAGTGGCATGCACCG 24367

RESULT 5
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LOCUS AY190942 44139 bp DNA linear INV 26-DEC-2002
DEFINITION Drosophila pseudoobscura clone DPSF01_33_N22 (D1412) genomic

sequence.

ACCESSION AY190942

VERSION AY190942.1 GI:27374267

KEYWORDS .

SOURCE Drosophila pseudoobscura

ORGANISM Drosophila pseudoobscura
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 44139)

AUTHORS Bergman,C.M., Pfeiffer,B.D., Rincon-Limas,D.E., Hoskins,R.A.,
Gnirke,A., Mungall,C.J., Wang,A.M., Kronmiller,B., Pacleb,J.,
Park,S., Stapleton,M., Wan,K., George,R.A., de Jong,P.J., Botas,J.,
Rubin,G.M. and Celniker,S.E.

TITLE Assessing the impact of comparative genomic sequence data on the
functional annotation of the Drosophila genome

JOURNAL Genome Biol. 3 (12), research0086 (2002)

REMARK <http://genomebiology.com/2002/3/12/research/0086>

REFERENCE 2 (bases 1 to 44139)

AUTHORS Pfeiffer,B.D., Bergman,C.M., Gnirke,A., Hoskins,R.A., Moshrefi,A.,
Mungall,C.J., Pacleb,J., Wang,A.M., Park,S., Wan,K., George,R.A.,
Rubin,G.M. and Celniker,S.E.

TITLE Direct Submission

JOURNAL Submitted (02-DEC-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, 1 Cyclotron Rd, Berkeley, CA
94720, USA

COMMENT Gene annotations are preliminary because they are based solely on
alignments of conceptually translated gene models to the
corresponding gene model in Drosophila melanogaster. As a
consequence we did not annotate UTRs. In choosing splice sites, we
maximized conservation of amino acids rather than adherence to
consensus splice site.

FEATURES Location/Qualifiers

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ORIGIN

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RESULT 6

AC158186/c

LOCUS AC158186 30844 bp DNA linear PLN 26-MAY-2005

DEFINITION Selaginella moellendorffii clone JGIASXY-5F17, complete sequence.

ACCESSION AC158186

VERSION AC158186.2 GI:66730719

KEYWORDS HTG.

SOURCE Selaginella moellendorffii

ORGANISM Selaginella moellendorffii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Lycopodiophyta; Isoetopsida; Selaginellales; Selaginellaceae;
 Selaginella.

REFERENCE 1 (bases 1 to 30844)

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 30844)

AUTHORS DOE Joint Genome Institute.

TITLE Direct Submission

JOURNAL Submitted (09-MAR-2005) Production Genomics Facility, DOE Joint
 Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA
 94598-1698, USA

REFERENCE 3 (bases 1 to 30844)

AUTHORS Stanford Human Genome Center.

CONSRTM DOE Joint Genome Institute

TITLE Direct Submission

JOURNAL Submitted (26-MAY-2005) DOE Joint Genome Institute, 2800 Mitchell
 Drive, Walnut Creek, CA 94598, USA

COMMENT On May 26, 2005 this sequence version replaced gi:60650325.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www-shgc.stanford.edu

Quality: Phrap Quality >=40 99.9% of Sequence;

Estimated Total Number of Errors is 0.

FEATURES Location/Qualifiers

source

1. .30844

/organism="Selaginella moellendorffii"

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ORIGIN

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 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTGGCAACAGTGGCATGCACCG 22
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RESULT 7

AL603830

LOCUS AL603830 104771 bp DNA linear ROD 09-FEB-2005

DEFINITION Mouse DNA sequence from clone RP23-467E19 on chromosome 11 Contains the Map2k3 gene for mitogen activated protein kinase kinase 3, the Gtlf3a gene for gene trap locus F3a, the Gtlf3b gene for gene trap locus F3b and two CpG islands, complete sequence.

ACCESSION AL603830

VERSION AL603830.7 GI:17017794

KEYWORDS HTG; CpG island; Gtlf3a; Gtlf3b; kinase; Map2K3.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 104771)

AUTHORS Clark, S.

TITLE Direct Submission

JOURNAL Submitted (04-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk

COMMENT On Nov 20, 2001 this sequence version replaced gi:16944205.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep -----
Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: vega@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.

RP23-467E19 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6.

FEATURES Location/Qualifiers

source

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